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(54) **Methods for accurate sequence data and modified base position determination**

(57) Disclosed herein are methods of determining the sequence and/or positions of modified bases in a nucleic acid sample present in a circular molecule with a nucleic acid insert of known sequence comprising obtaining sequence data of at least two insert-sample units. In some embodiments, the methods comprise obtaining sequence data using circular pair-locked molecules. In some embodiments, the methods comprise calculating scores of sequences of the nucleic acid inserts by comparing the sequences to the known sequence of the nucleic acid insert, and accepting or rejecting repeats of the sequence of the nucleic acid sample according to the scores of one or both of the sequences of the inserts immediately upstream or downstream of the repeats of the sequence of the nucleic acid sample.

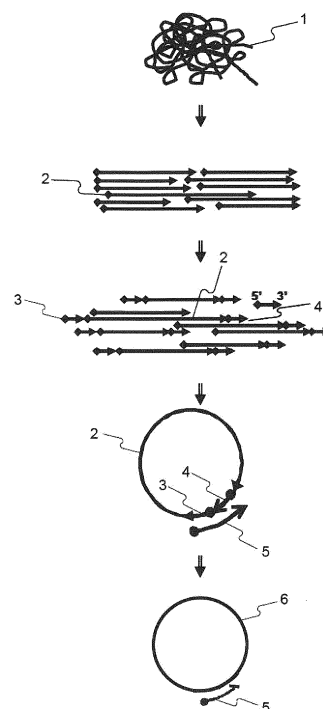


Fig. 1



EUROPEAN SEARCH REPORT

Application Number
EP 14 15 0163

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